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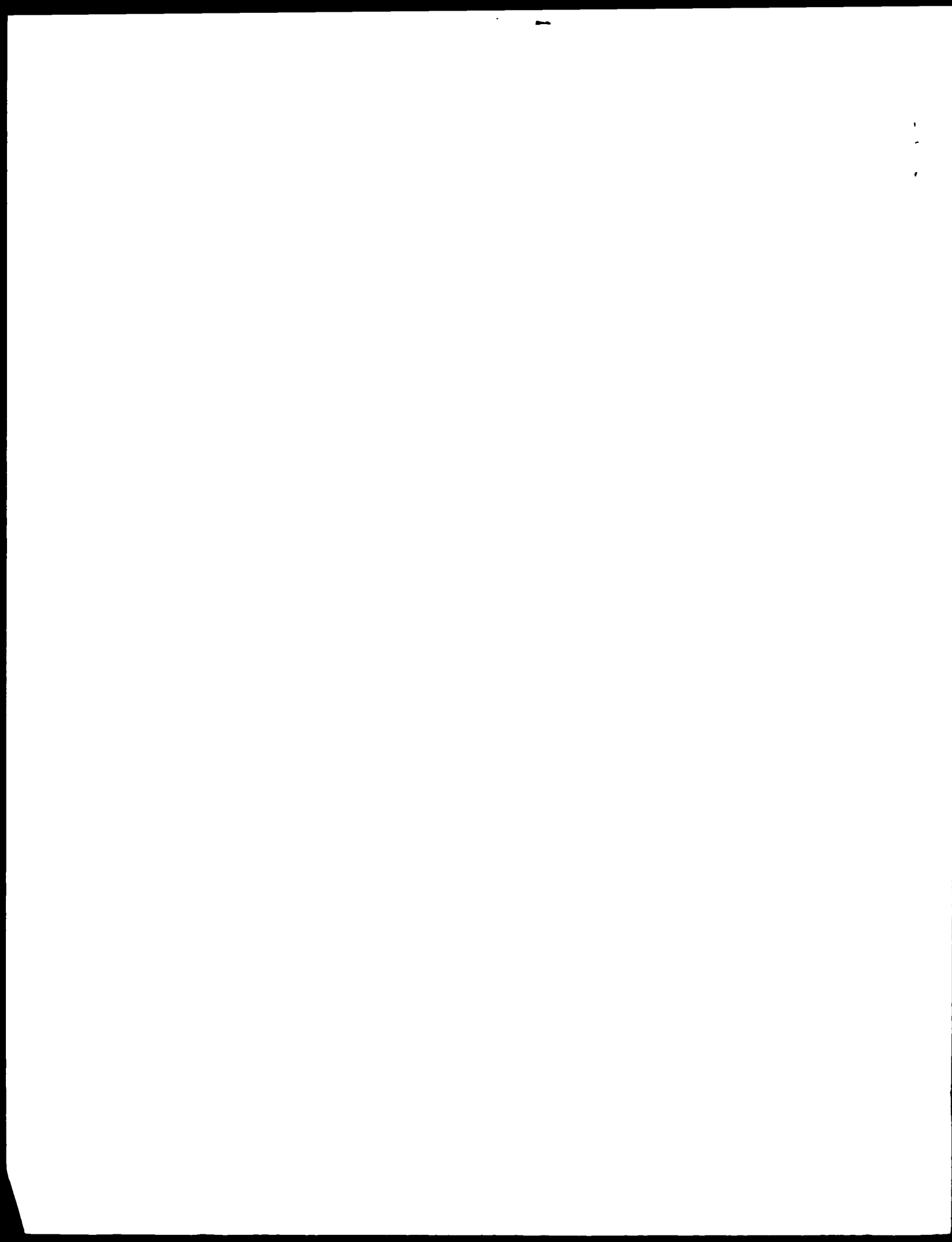
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TYPE OF SEARCH:
NA Sequences: 7
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Structures: _____
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Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
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1. The first group of variables includes the demographic characteristics of the respondents, such as age, gender, and education level. These variables are used to control for potential confounding factors that may influence the relationship between the independent and dependent variables.

2. The second group of variables represents the independent variables, which are the factors being manipulated or measured in the study. These variables are hypothesized to have a direct effect on the dependent variable.

3. The third group of variables includes the control variables, which are used to account for other factors that may influence the outcome. These variables are typically measured at the same time as the independent variables to ensure that any observed effects are due to the independent variables and not other factors.

4. The final group of variables represents the dependent variable, which is the outcome or result of the study. This variable is the primary focus of the research and is used to assess the impact of the independent variables.

Overall, the study aims to explore the relationship between the independent variables and the dependent variable, while controlling for potential confounding factors. The results of the study will provide valuable insights into the factors that influence the outcome and help inform future research and practice.

biochemical and molecular biology of the cell cycle.

Case	α	β	γ	δ	ϵ	ζ	η	θ	ι	κ	λ	μ	ν	ξ	\omicron	π	ρ	σ	τ	υ	ϕ	χ	ψ	ω
1	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
2	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
3	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
4	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
5	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
6	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
7	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
8	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
9	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
10	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
11	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
12	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
13	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
14	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
15	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
16	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4
17	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1													

the effect of the β parameter on the α parameter.

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1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 26

[illegible]

1. *Journal of the American Statistical Association*, 1994, 89, 1033-1041.

[illegible]

Journal of Management Studies, 19(1), 67-80.

[illegible]

1. $\mathcal{A} = \{A_1, A_2, \dots, A_n\}$ is a family of sets.

[illegible]

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration was adjusted to 10⁸ cells/ml. The cells were then mixed with the plant tissue and incubated for 24 h at 28 °C. The plant tissue was then cultured on the selective medium. The transformation efficiency was determined as the number of transformants per 10⁶ cells. The data are the mean ± SD of three independent experiments.

$$f_{\lambda} = \frac{1}{2} \left(\frac{1}{\lambda} + \lambda \right) \quad \text{and} \quad K_{\lambda} = \frac{1}{2} \left(\frac{1}{\lambda} - \lambda \right).$$

Now, we consider the case $\alpha = 0$. Then, \mathcal{H}_0 is the set of all functions f satisfying

[illegible]

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration was adjusted to 10⁸ cells/ml. The cells were then mixed with the plant tissue and the transformation efficiency was determined. The results are shown as the mean ± SD of three independent experiments. The asterisk indicates a significant difference (p < 0.05) between the control and the treated groups.

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12. Claim 29 is SEQ ID No 49, or 49 part. End of text.

XX the present invention relates to a human single exon nucleic acid probes (SNPs). The present sequence is one such probe. The SNPs are derived from human beta cell. The SNPs can be used to produce a single exon nucleic acid probes, which can be used for measuring human gene expression in a sample derived from human beta cell epithelial cells. By measuring gene expression, the probes are useful in studying and/or studying of diseases of the beta cell, not only oral cancer.

XX. Note the sequence of this patent did not form part of the prior art information, but was obtained in electronic format directly from where it was published.

XX. The probe is a single exon nucleic acid probes.

XX. Sequence 49, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000.

12. Claim 29 is SEQ ID No 49, or 49 part. End of text.

XX the present invention relates to a human single exon nucleic acid probes (SNPs). The present sequence is one such probe. The SNPs are derived from human beta cell. The SNPs can be used to produce a single exon nucleic acid probes, which can be used for measuring human gene expression in a sample derived from human beta cell epithelial cells. By measuring gene expression, the probes are useful in studying and/or studying of diseases of the beta cell, not only oral cancer.

XX. Note the sequence of this patent did not form part of the prior art information, but was obtained in electronic format directly from where it was published.

XX. The probe is a single exon nucleic acid probes.

XX. Sequence 49, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000.

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Barth, S., 2002, *Journal of Statistical Software*, 20: 7-42. *Seconds (without alignment)*
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1. *Introduction*
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 3. *Methodology*
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Symbol	Meaning
\mathbb{R}	Real numbers
\mathbb{Z}	Integers
\mathbb{N}	Natural numbers
\mathbb{Q}	Rational numbers
\mathbb{C}	Complex numbers
\mathbb{H}	Quaternions
\mathbb{O}	Octonions
\mathbb{K}	Field
\mathbb{F}	Field
\mathbb{A}	Algebra
\mathbb{M}	Module
\mathbb{V}	Vector space
\mathbb{W}	Subspace
\mathbb{U}	Unitary group
$\mathbb{O}(n)$	Orthogonal group
$\mathbb{S}(n)$	Special orthogonal group
$\mathbb{U}(n)$	Unitary group
$\mathbb{S}(n)$	Special unitary group
$\mathbb{H}(n)$	Quaternionic unitary group
$\mathbb{O}(n)$	Octonionic unitary group
$\mathbb{K}(n)$	Field unitary group
$\mathbb{F}(n)$	Field unitary group
$\mathbb{A}(n)$	Algebra unitary group
$\mathbb{M}(n)$	Module unitary group
$\mathbb{V}(n)$	Vector space unitary group
$\mathbb{W}(n)$	Subspace unitary group
$\mathbb{U}(n, \mathbb{K})$	Unitary group over field \mathbb{K}
$\mathbb{S}(n, \mathbb{K})$	Special unitary group over field \mathbb{K}
$\mathbb{H}(n, \mathbb{K})$	Quaternionic unitary group over field \mathbb{K}
$\mathbb{O}(n, \mathbb{K})$	Octonionic unitary group over field \mathbb{K}
$\mathbb{K}(n, \mathbb{K})$	Field unitary group over field \mathbb{K}
$\mathbb{F}(n, \mathbb{K})$	Field unitary group over field \mathbb{K}
$\mathbb{A}(n, \mathbb{K})$	Algebra unitary group over field \mathbb{K}
$\mathbb{M}(n, \mathbb{K})$	Module unitary group over field \mathbb{K}
$\mathbb{V}(n, \mathbb{K})$	Vector space unitary group over field \mathbb{K}
$\mathbb{W}(n, \mathbb{K})$	Subspace unitary group over field \mathbb{K}
$\mathbb{U}(n, \mathbb{K}, \mathbb{L})$	Unitary group over field \mathbb{K} and \mathbb{L}
$\mathbb{S}(n, \mathbb{K}, \mathbb{L})$	Special unitary group over field \mathbb{K} and \mathbb{L}
$\mathbb{H}(n, \mathbb{K}, \mathbb{L})$	Quaternionic unitary group over field \mathbb{K} and \mathbb{L}
$\mathbb{O}(n, \mathbb{K}, \mathbb{L})$	Octonionic unitary group over field \mathbb{K} and \mathbb{L}
$\mathbb{K}(n, \mathbb{K}, \mathbb{L})$	Field unitary group over field \mathbb{K} and \mathbb{L}
$\mathbb{F}(n, \mathbb{K}, \mathbb{L})$	Field unitary group over field \mathbb{K} and \mathbb{L}
$\mathbb{A}(n, \mathbb{K}, \mathbb{L})$	Algebra unitary group over field \mathbb{K} and \mathbb{L}
$\mathbb{M}(n, \mathbb{K}, \mathbb{L})$	Module unitary group over field \mathbb{K} and \mathbb{L}
$\mathbb{V}(n, \mathbb{K}, \mathbb{L})$	Vector space unitary group over field \mathbb{K} and \mathbb{L}
$\mathbb{W}(n, \mathbb{K}, \mathbb{L})$	Subspace unitary group over field \mathbb{K} and \mathbb{L}
$\mathbb{U}(n, \mathbb{K}, \mathbb{L}, \mathbb{M})$	Unitary group over field \mathbb{K} , \mathbb{L} and \mathbb{M}
$\mathbb{S}(n, \mathbb{K}, \mathbb{L}, \mathbb{M})$	Special unitary group over field \mathbb{K} , \mathbb{L} and \mathbb{M}
$\mathbb{H}(n, \mathbb{K}, \mathbb{L}, \mathbb{M})$	Quaternionic unitary group over field \mathbb{K} , \mathbb{L} and \mathbb{M}
$\mathbb{O}(n, \mathbb{K}, \mathbb{L}, \mathbb{M})$	Octonionic unitary group over field \mathbb{K} , \mathbb{L} and \mathbb{M}
$\mathbb{K}(n, \mathbb{K}, \mathbb{L}, \mathbb{M})$	Field unitary group over field \mathbb{K} , \mathbb{L} and \mathbb{M}
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$\mathbb{A}(n, \mathbb{K}, \mathbb{L}, \mathbb{M})$	Algebra unitary group over field \mathbb{K} , \mathbb{L} and \mathbb{M}
$\mathbb{M}(n, \mathbb{K}, \mathbb{L}, \mathbb{M})$	Module unitary group over field \mathbb{K} , \mathbb{L} and \mathbb{M}
$\mathbb{V}(n, \mathbb{K}, \mathbb{L}, \mathbb{M})$	Vector space unitary group over field \mathbb{K} , \mathbb{L} and \mathbb{M}
$\mathbb{W}(n, \mathbb{K}, \mathbb{L}, \mathbb{M})$	Subspace unitary group over field \mathbb{K} , \mathbb{L} and \mathbb{M}
$\mathbb{U}(n, \mathbb{K}, \mathbb{L}, \mathbb{M}, \mathbb{N})$	Unitary group over field \mathbb{K} , \mathbb{L} , \mathbb{M} and \mathbb{N}
$\mathbb{S}(n, \mathbb{K}, \mathbb{L}, \mathbb{M}, \mathbb{N})$	Special unitary group over field \mathbb{K} , \mathbb{L} , \mathbb{M} and \mathbb{N}
$\mathbb{H}(n, \mathbb{K}, \mathbb{L}, \mathbb{M}, \mathbb{N})$	Quaternionic unitary group over field \mathbb{K} , \mathbb{L} , \mathbb{M} and \mathbb{N}
$\mathbb{O}(n, \mathbb{K}, \mathbb{L}, \mathbb{M}, \mathbb{N})$	Octonionic unitary group over field \mathbb{K} , \mathbb{L} , \mathbb{M} and \mathbb{N}
$\mathbb{K}(n, \mathbb{K}, \mathbb{L}, \mathbb{M}, \mathbb{N})$	Field unitary group over field \mathbb{K} , \mathbb{L} , \mathbb{M} and \mathbb{N}
$\mathbb{F}(n, \mathbb{K}, \mathbb{L}, \mathbb{M}, \mathbb{N})$	Field unitary group over field \mathbb{K} , \mathbb{L} , \mathbb{M} and \mathbb{N}
$\mathbb{A}(n, \mathbb{K}, \mathbb{L}, \mathbb{M}, \mathbb{N})$	Algebra unitary group over field \mathbb{K} , \mathbb{L} , \mathbb{M} and \mathbb{N}
$\mathbb{M}(n, \mathbb{K}, \mathbb{L}, \mathbb{M}, \mathbb{N})$	Module unitary group over field \mathbb{K} , \mathbb{L} , \mathbb{M} and \mathbb{N}
$\mathbb{V}(n, \mathbb{K}, \mathbb{L}, \mathbb{M}, \mathbb{N})$	Vector space unitary group over field \mathbb{K} , \mathbb{L} , \mathbb{M} and \mathbb{N}
$\mathbb{W}(n, \mathbb{K}, \mathbb{L}, \mathbb{M}, \mathbb{N})$	Subspace unitary group over field \mathbb{K} , \mathbb{L} , \mathbb{M} and \mathbb{N}

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$$L^2(\mathbb{R}^n) \rightarrow L^2(\mathbb{R}^n) \quad \text{by} \quad f \mapsto \int_{\mathbb{R}^n} f(x) dx \quad \star$$
[illegible]

Case	Age	Sex	Site	Pathologic Findings	Immunohistochemical Findings	Outcome
1	65	M	Rectum	Adenocarcinoma	CD117 (+), CD34 (+), CD56 (-), CD117/CD34 ratio = 1.0	Survived 12 months
2	72	F	Rectum	Adenocarcinoma	CD117 (+), CD34 (+), CD56 (-), CD117/CD34 ratio = 1.0	Survived 18 months
3	68	M	Rectum	Adenocarcinoma	CD117 (+), CD34 (+), CD56 (-), CD117/CD34 ratio = 1.0	Survived 24 months
4	70	F	Rectum	Adenocarcinoma	CD117 (+), CD34 (+), CD56 (-), CD117/CD34 ratio = 1.0	Survived 30 months
5	75	M	Rectum	Adenocarcinoma	CD117 (+), CD34 (+), CD56 (-), CD117/CD34 ratio = 1.0	Survived 36 months
6	78	F	Rectum	Adenocarcinoma	CD117 (+), CD34 (+), CD56 (-), CD117/CD34 ratio = 1.0	Survived 42 months
7	80	M	Rectum	Adenocarcinoma	CD117 (+), CD34 (+), CD56 (-), CD117/CD34 ratio = 1.0	Survived 48 months
8	82	F	Rectum	Adenocarcinoma	CD117 (+), CD34 (+), CD56 (-), CD117/CD34 ratio = 1.0	Survived 54 months
9	85	M	Rectum	Adenocarcinoma	CD117 (+), CD34 (+), CD56 (-), CD117/CD34 ratio = 1.0	Survived 60 months
10	88	F	Rectum	Adenocarcinoma	CD117 (+), CD34 (+), CD56 (-), CD117/CD34 ratio = 1.0	Survived 66 months

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Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (C) and the experimental group (E). The control group (C) was divided into two subgroups: the control group (C) and the control group (C). The experimental group (E) was divided into two subgroups: the experimental group (E) and the experimental group (E). The control group (C) was divided into two subgroups: the control group (C) and the control group (C). The experimental group (E) was divided into two subgroups: the experimental group (E) and the experimental group (E).

1. *Staphylococcus aureus* (Staph. aureus) is the most common cause of skin infections. It is a gram-positive, spherical bacterium that can form clusters. It is often found on the skin and in the nose.

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Country	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)	Population growth rate (%)	Urban population growth rate (%)	Population growth rate (%)	Urban population growth rate (%)
Algeria	1980	10.0	4.0	40.0	100	400	1.5	2.5	1.5	2.5
Algeria	1985	10.5	4.5	42.9	105	450	1.8	2.8	1.8	2.8
Algeria	1990	11.0	5.0	45.5	110	500	2.0	3.0	2.0	3.0
Algeria	1995	11.5	5.5	47.8	115	550	2.2	3.2	2.2	3.2
Algeria	2000	12.0	6.0	50.0	120	600	2.5	3.5	2.5	3.5
Algeria	2005	12.5	6.5	52.0	125	650	2.8	3.8	2.8	3.8
Algeria	2010	13.0	7.0	53.8	130	700	3.0	4.0	3.0	4.0
Algeria	2015	13.5	7.5	55.6	135	750	3.2	4.2	3.2	4.2
Algeria	2020	14.0	8.0	57.1	140	800	3.5	4.5	3.5	4.5
Algeria	2025	14.5	8.5	58.6	145	850	3.8	4.8	3.8	4.8
Algeria	2030	15.0	9.0	60.0	150	900	4.0	5.0	4.0	5.0
Algeria	2035	15.5	9.5	61.3	155	950	4.2	5.2	4.2	5.2
Algeria	2040	16.0	10.0	62.5	160	1000	4.5	5.5	4.5	5.5
Algeria	2045	16.5	10.5	63.6	165	1050	4.8	5.8	4.8	5.8
Algeria	2050	17.0	11.0	64.7	170	1100	5.0	6.0	5.0	6.0
Algeria	2055	17.5	11.5	65.7	175	1150	5.2	6.2	5.2	6.2
Algeria	2060	18.0	12.0	66.7	180	1200	5.5	6.5	5.5	6.5
Algeria	2065	18.5	12.5	67.6	185	1250	5.8	6.8	5.8	6.8
Algeria	2070	19.0	13.0	68.4	190	1300	6.0	7.0	6.0	7.0
Algeria	2075	19.5	13.5	69.2	195	1350	6.2	7.2	6.2	7.2
Algeria	2080	20.0	14.0	70.0	200	1400	6.5	7.5	6.5	7.5
Algeria	2085	20.5	14.5	70.7	205	1450	6.8	7.8	6.8	7.8
Algeria	2090	21.0	15.0	71.4	210	1500	7.0	8.0	7.0	8.0
Algeria	2095	21.5	15.5	72.1	215	1550	7.2	8.2	7.2	8.2
Algeria	2100	22.0	16.0	72.7	220	1600	7.5	8.5	7.5	8.5
Algeria	2105	22.5	16.5	73.3	225	1650	7.8	8.8	7.8	8.8
Algeria	2110	23.0	17.0	73.9	230	1700	8.0	9.0	8.0	9.0
Algeria	2115	23.5	17.5	74.5	235	1750	8.2	9.2	8.2	9.2
Algeria	2120	24.0	18.0	75.0	240	1800	8.5	9.5	8.5	9.5
Algeria	2125	24.5	18.5	75.5	245	1850	8.8	9.8	8.8	9.8
Algeria	2130	25.0	19.0	76.0	250	1900	9.0	10.0	9.0	10.0
Algeria	2135	25.5	19.5	76.5	255	1950	9.2	10.2	9.2	10.2
Algeria	2140	26.0	20.0	76.9	260	2000	9.5	10.5	9.5	10.5
Algeria	2145	26.5	20.5	77.3	265	2050	9.8	10.8	9.8	10.8
Algeria	2150	27.0	21.0	77.8	270	2100	10.0	11.0	10.0	11.0
Algeria	2155	27.5	21.5	78.2	275	2150	10.2	11.2		

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Case	Age	Sex	Site	Pathologic	Survival
1	60	M	Rectum	Adenocarcinoma	10 years
2	65	F	Rectum	Adenocarcinoma	12 years
3	70	M	Rectum	Adenocarcinoma	15 years
4	75	F	Rectum	Adenocarcinoma	18 years
5	80	M	Rectum	Adenocarcinoma	20 years
6	85	F	Rectum	Adenocarcinoma	22 years
7	90	M	Rectum	Adenocarcinoma	25 years
8	95	F	Rectum	Adenocarcinoma	28 years
9	100	M	Rectum	Adenocarcinoma	30 years
10	105	F	Rectum	Adenocarcinoma	32 years

NOTES

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the β phase of the polymer. The β phase is the more ordered phase and is characterized by a higher density and a higher melting point than the α phase. The β phase is also the more stable phase and is the one that is most commonly observed in nature. The α phase is the less ordered phase and is characterized by a lower density and a lower melting point than the β phase. The α phase is also the less stable phase and is the one that is most commonly observed in nature.

$$\begin{aligned} \mathbb{E}[\mathcal{L}_{\text{train}}] &= \mathbb{E}[\mathcal{L}_{\text{train}}(\mathbf{w})] = \mathbb{E}[\mathcal{L}_{\text{train}}(\mathbf{w}^*)] + \mathbb{E}[\mathcal{L}_{\text{train}}(\mathbf{w}) - \mathcal{L}_{\text{train}}(\mathbf{w}^*)] \\ &= \mathbb{E}[\mathcal{L}_{\text{train}}(\mathbf{w}^*)] + \mathbb{E}[\mathcal{L}_{\text{train}}(\mathbf{w}) - \mathcal{L}_{\text{train}}(\mathbf{w}^*)] \\ &= \mathbb{E}[\mathcal{L}_{\text{train}}(\mathbf{w}^*)] + \mathbb{E}[\mathcal{L}_{\text{train}}(\mathbf{w}) - \mathcal{L}_{\text{train}}(\mathbf{w}^*)] \end{aligned}$$

The diagram illustrates the experimental design. It shows a sequence of events: a stimulus is presented, a response is recorded, and the response is evaluated. This process is repeated for multiple trials. The diagram is labeled with 'Stimulus', 'Response', and 'Evaluation'.

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- Center, Washington University Genome Sequencing Center
 Center, code: WUSG
 Web site: <http://pc2222.wustl.edu/genome/seq/seq.html>
 Center project name: H_Mindgulf5

- * Note: This is a "working draft" sequence. It currently
 consists of 46 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N. But the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * As soon as it is available and the accession number will
 be provided.

- 1372 12713 gap of unknown length
 1373 26961 gap of 1619 bp in length
 2691 26961 gap of unknown length
 2691 44723 gap of 1482 bp in length
 4473 45723 gap of unknown length
 4573 58563 gap of 1278 bp in length
 5851 60563 gap of unknown length
 6051 72923 gap of 1642 bp in length
 7293 73923 gap of unknown length
 7393 84283 gap of 1936 bp in length
 8429 112953 gap of 1657 bp in length
 11296 132233 gap of unknown length
 13186 132233 gap of 1742 bp in length
 13238 145733 gap of unknown length
 14531 145733 gap of 1543 bp in length
 14571 169123 gap of 1672 bp in length
 16913 176983 gap of 1241 bp in length
 17684 176983 gap of unknown length
 17684 187733 gap of 1514 bp in length
 18798 187733 gap of unknown length
 18798 197733 gap of 1678 bp in length
 19796 213733 gap of unknown length
 21396 214733 gap of 1715 bp in length
 21491 234733 gap of unknown length
 23491 254733 gap of 1680 bp in length
 25491 274733 gap of unknown length
 27491 294733 gap of 1526 bp in length
 29491 314733 gap of unknown length
 31491 334733 gap of 2784 bp in length
 33491 354733 gap of unknown length
 35491 374733 gap of 2215 bp in length
 37491 394733 gap of unknown length
 39491 414733 gap of 2022 bp in length
 41491 434733 gap of unknown length
 43491 454733 gap of 1936 bp in length
 45491 474733 gap of unknown length
 47491 494733 gap of 2446 bp in length
 49491 514733 gap of unknown length
 51491 534733 gap of 2201 bp in length
 53491 554733 gap of unknown length

TABLE 1

Accession	Contig	Length	Assembly
U000000.1	U000000.1	1372	U000000.1
U000000.1	U000000.1	2691	U000000.1
U000000.1	U000000.1	4473	U000000.1
U000000.1	U000000.1	5851	U000000.1
U000000.1	U000000.1	7293	U000000.1
U000000.1	U000000.1	8429	U000000.1
U000000.1	U000000.1	11296	U000000.1
U000000.1	U000000.1	13186	U000000.1
U000000.1	U000000.1	14531	U000000.1
U000000.1	U000000.1	16913	U000000.1
U000000.1	U000000.1	17684	U000000.1
U000000.1	U000000.1	18798	U000000.1
U000000.1	U000000.1	19796	U000000.1
U000000.1	U000000.1	21396	U000000.1
U000000.1	U000000.1	23491	U000000.1
U000000.1	U000000.1	25491	U000000.1
U000000.1	U000000.1	27491	U000000.1
U000000.1	U000000.1	29491	U000000.1
U000000.1	U000000.1	31491	U000000.1
U000000.1	U000000.1	33491	U000000.1
U000000.1	U000000.1	35491	U000000.1
U000000.1	U000000.1	37491	U000000.1
U000000.1	U000000.1	39491	U000000.1
U000000.1	U000000.1	41491	U000000.1
U000000.1	U000000.1	43491	U000000.1
U000000.1	U000000.1	45491	U000000.1
U000000.1	U000000.1	47491	U000000.1
U000000.1	U000000.1	49491	U000000.1
U000000.1	U000000.1	51491	U000000.1
U000000.1	U000000.1	53491	U000000.1
U000000.1	U000000.1	55491	U000000.1

Genome version 4.5
Copyright (c) 1993-2000 Compugen Ltd.

AM nucleic nucleic seqs, using model

Run on: March 3, 2002, 02:11:28 : Search time 2037.42 seconds
(without alignments)
145,748 million cell updates/sec

Title: US-09-863-777-7

Perfected source: 18

Sequences: 1 decontaminated 18

Scoring table: IDENTITY_N92

Gapop (in %): Gapext 1.0

Searched: 1472147 seqs, 8243589756 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum 100 seq length: 0

Maximum 100 seq length: 20000000

Post processing: Minimum Match 2%

Maximum Match 100%

Listed first 45 summaries

Paradise:

GenBank:

1: gb_bat*

2: gb_bat*

3: gb_bat*

4: gb_bat*

5: gb_bat*

6: gb_bat*

7: gb_bat*

8: gb_bat*

9: gb_bat*

10: gb_bat*

11: gb_bat*

12: gb_bat*

13: gb_bat*

14: gb_bat*

15: gb_bat*

16: gb_bat*

17: gb_bat*

18: gb_bat*

19: gb_bat*

20: gb_bat*

21: gb_bat*

22: gb_bat*

23: gb_bat*

24: gb_bat*

25: gb_bat*

26: gb_bat*

27: gb_bat*

28: gb_bat*

29: gb_bat*

30: gb_bat*

31: gb_bat*

32: gb_bat*

33: gb_bat*

34: gb_bat*

35: gb_bat*

36: gb_bat*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9

Entry No.	Score	Query Match	Length	PP	IT	Accession
1	16.4	100.0	1797	5	100.000	U01963
2	16.4	100.0	4419	5	94.880	M17117
3	16.4	100.0	20367	4	93.880	M17117
4	16.4	94.4	42008	2	87.100	A01100
5	16.4	94.4	18246	2	87.100	A01100
6	16.4	94.4	13946	2	87.100	A01100
7	16.4	94.4	16253	2	87.100	A01100
8	16.4	94.4	17947	2	87.100	A01100
9	16.4	94.4	18449	2	87.100	A01100
10	16.4	94.4	18963	2	87.100	A01100
11	16.4	94.4	19196	2	87.100	A01100
12	16.4	94.4	21742	2	87.100	A01100
13	16.4	94.4	417	5	87.100	A01100
14	16.4	94.4	417	5	87.100	A01100
15	16.4	94.4	417	5	87.100	A01100
16	16.4	94.4	417	5	87.100	A01100
17	16.4	94.4	417	5	87.100	A01100
18	16.4	94.4	417	5	87.100	A01100
19	16.4	94.4	417	5	87.100	A01100
20	16.4	94.4	417	5	87.100	A01100
21	16.4	94.4	417	5	87.100	A01100
22	16.4	94.4	417	5	87.100	A01100
23	16.4	94.4	417	5	87.100	A01100
24	16.4	94.4	417	5	87.100	A01100
25	16.4	94.4	417	5	87.100	A01100
26	16.4	94.4	417	5	87.100	A01100
27	16.4	94.4	417	5	87.100	A01100
28	16.4	94.4	417	5	87.100	A01100
29	16.4	94.4	417	5	87.100	A01100
30	16.4	94.4	417	5	87.100	A01100
31	16.4	94.4	417	5	87.100	A01100
32	16.4	94.4	417	5	87.100	A01100
33	16.4	94.4	417	5	87.100	A01100
34	16.4	94.4	417	5	87.100	A01100
35	16.4	94.4	417	5	87.100	A01100
36	16.4	94.4	417	5	87.100	A01100
37	16.4	94.4	417	5	87.100	A01100
38	16.4	94.4	417	5	87.100	A01100
39	16.4	94.4	417	5	87.100	A01100
40	16.4	94.4	417	5	87.100	A01100
41	16.4	94.4	417	5	87.100	A01100
42	16.4	94.4	417	5	87.100	A01100
43	16.4	94.4	417	5	87.100	A01100
44	16.4	94.4	417	5	87.100	A01100
45	16.4	94.4	417	5	87.100	A01100

Accession

Accession	Score	Query Match	Length	PP	IT	Accession
U01963	100.0	100.0	1797	5	100.000	U01963
Sequence 2 from Table 1	94.880	94.880	4419	5	94.880	U01963
Sequence 3 from Table 1	93.880	93.880	20367	4	93.880	U01963
Sequence 4 from Table 1	87.100	87.100	42008	2	87.100	U01963
Sequence 5 from Table 1	87.100	87.100	18246	2	87.100	U01963
Sequence 6 from Table 1	87.100	87.100	13946	2	87.100	U01963
Sequence 7 from Table 1	87.100	87.100	16253	2	87.100	U01963
Sequence 8 from Table 1	87.100	87.100	17947	2	87.100	U01963
Sequence 9 from Table 1	87.100	87.100	18449	2	87.100	U01963
Sequence 10 from Table 1	87.100	87.100	18963	2	87.100	U01963
Sequence 11 from Table 1	87.100	87.100	19196	2	87.100	U01963
Sequence 12 from Table 1	87.100	87.100	21742	2	87.100	U01963
Sequence 13 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 14 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 15 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 16 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 17 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 18 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 19 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 20 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 21 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 22 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 23 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 24 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 25 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 26 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 27 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 28 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 29 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 30 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 31 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 32 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 33 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 34 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 35 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 36 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 37 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 38 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 39 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 40 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 41 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 42 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 43 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 44 from Table 1	87.100	87.100	417	5	87.100	U01963
Sequence 45 from Table 1	87.100	87.100	417	5	87.100	U01963


```

STS      126523 132181
Zoo: "matched EMBL:172921
RHH:RHH05414
RHH:RHH056
dBS:STS27216
Identified using the e-PCR software (G. Schuler)"
133203 132123
Zoo: "matched EMBL:1037931
RHH:RHH11266
dBS:STS46764
Identified using the e-PCR software (G. Schuler)"
132833 132360
Zoo: "matched EMBL:452605
RHH:RHH09454
dBS:STS46671
Identified using the e-PCR software (G. Schuler)"
132471 132577
Zoo: "matched EMBL:511466
RHH:RHH05428
RHH:RHH1937
dBS:STS24066
Identified using the e-PCR software (G. Schuler)"
132481 132622
Zoo: "matched EMBL:520814
RHH:RHH1727
dBS:STS18432
Identified using the e-PCR software (G. Schuler)"
133060 133178
Zoo: "matched EMBL:332523
RHH:RHH07214
dBS:STS184711
Identified using the e-PCR software (G. Schuler)"
181439 131715
Zoo: "matched EMBL:X76884
RHH:RHH0907
dBS:STS56073
Identified using the e-PCR software (G. Schuler)"
BASE CONT 136613 132243 456223 577233
SEQUIN

query Match 100.00 Score 181 Length 204673
Best Local Similarity 100.00 Prod. No. 310002
Matches 181 Conservative 07 Mismatches 07 Indels 07 Gaps 07

CV 1 accuracy 100.00
11111111111111111111
DB 132021 AAAAAATTATATCTA 125503

RESULT 4
LOCUS      A018022 42096 bp 181 09-DEC-1999
DEFINITION Protophila melanosticta. *** SEQUENCING IN PROGRESS ***. In ordered
pieces.
VERSION    A018022
KEYWORDS   HTG; HTGS_PHASE1;
SOURCE     Tritic Tly.
ORGANISM   Protophila melanosticta
Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
Procyota; Neoptera; Endopterygota; Diptera; Brachycera;
Mesomorpha; Ephyridiidae; Protophiliidae; Protophila.
1 (bases 1 to 42096)
Adams, M. and Venturi, J. C.
Direct Submission
Submitted (09-DEC-1999) GenBank, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as A018022065 by the submitter.
For more information on this record e-mail to tly@celera.com.
* Note: this is a "sinking trail" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and

```

```

FEATURES
Source
1..42096
Zoo: "matched EMBL:172921
RHH:RHH05414
RHH:RHH056
dBS:STS27216
Identified using the e-PCR software (G. Schuler)"
133203 132123
Zoo: "matched EMBL:1037931
RHH:RHH11266
dBS:STS46764
Identified using the e-PCR software (G. Schuler)"
132833 132360
Zoo: "matched EMBL:452605
RHH:RHH09454
dBS:STS46671
Identified using the e-PCR software (G. Schuler)"
132471 132577
Zoo: "matched EMBL:511466
RHH:RHH05428
RHH:RHH1937
dBS:STS24066
Identified using the e-PCR software (G. Schuler)"
132481 132622
Zoo: "matched EMBL:520814
RHH:RHH1727
dBS:STS18432
Identified using the e-PCR software (G. Schuler)"
133060 133178
Zoo: "matched EMBL:332523
RHH:RHH07214
dBS:STS184711
Identified using the e-PCR software (G. Schuler)"
181439 131715
Zoo: "matched EMBL:X76884
RHH:RHH0907
dBS:STS56073
Identified using the e-PCR software (G. Schuler)"
BASE CONT 136613 132243 456223 577233
SEQUIN

query Match 100.00 Score 181 Length 204673
Best Local Similarity 100.00 Prod. No. 310002
Matches 181 Conservative 07 Mismatches 07 Indels 07 Gaps 07

CV 1 accuracy 100.00
11111111111111111111
DB 132021 AAAAAATTATATCTA 125503

RESULT 4
LOCUS      A018022 42096 bp 181 09-DEC-1999
DEFINITION Protophila melanosticta. *** SEQUENCING IN PROGRESS ***. In ordered
pieces.
VERSION    A018022
KEYWORDS   HTG; HTGS_PHASE1;
SOURCE     Tritic Tly.
ORGANISM   Protophila melanosticta
Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
Procyota; Neoptera; Endopterygota; Diptera; Brachycera;
Mesomorpha; Ephyridiidae; Protophiliidae; Protophila.
1 (bases 1 to 42096)
Adams, M. and Venturi, J. C.
Direct Submission
Submitted (09-DEC-1999) GenBank, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as A018022065 by the submitter.
For more information on this record e-mail to tly@celera.com.
* Note: this is a "sinking trail" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and

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KEYWORDS

GENUS
BOMOSAPIDENS

REFERENCES

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

1: 191909

Zodionism "Homo sapiens"

Zodionism "Homo sapiens"

Zodionism "Homo sapiens"

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Zodionism "Homo sapiens"

XX New nucleotide (s) that inhibit expression of antiogenin - for
 treatment of tumors and metastases, or other conditions involving
 abnormal angiogenesis

PS Chain 1: (see 38: 21pp): English.

XX Anti-sense phosphorothioate oligonucleotide (PS) encompasses the
 TATA box site, the human antiogenin gene (see AAV60914), JPRS,
 and other related and isopropylated bases (see AAV60911-17) with
 base sequences complementary to a target region of the antiogenin
 gene, are able to inhibit expression of antiogenin. They are used
 in claimed methods to decrease promotion of angiogenesis,
 particularly to reduce the size of tumors associated with
 angiogenesis, to inhibit metastases, establishment of tumor cells
 or growth of tumors and, when labeled, to detect antiogenin for
 diagnosis of conditions associated with abnormal angiogenesis.
 They can also be used to treat a wide range of non-cancer
 conditions that involve angiogenesis, e.g., are related macular
 degeneration, diabetic retinopathy, bacterial or fungal ulcers,
 rheumatoid arthritis, period's disease, Crohn's disease, haemorrhoids
 and many others listed.

XX Sequence 18 (B): 7 A: 3 C: 3 G: 6 T: 0 other:

Query Match: 100.0%; Score 18: 100.0; Length 18:
 Best Local Similarity: 100.0%; Fred. No. 42;

Matches 18: Conserved: 0; Mismatches 0; Indels 0; Gaps 0;

27 1 accaaattatattatctta 18
 111111111111111111

18 1 accaaattatattatctta 18

RESULTS:

AAV10047:

10 AAV10047 Standard, DNA, (see 10).

XX AAV10047:

XX AAV10047:

XX AAV10047 (First entry)

XX AAV10047 sequence encoding antiogenin in Lambda HAT 1.

XX AAV10047 repeat region

XX AAV10047 repeat region

XX AAV10047 repeat region

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XX AAV10047 repeat region

[illegible]

Library: March
 Vol. 182; Series: 16, 4; DB: B; Length: 3096;
 Postcode: Similarity: Vol. 182; Prod. No.: 382

(400)

FEATURES
SOURCE

Location/Zip/Comments

1. 11/10/01

Location/Zip/Comments

Zip 10001 "New York"

Zip 10001 "New York"

Zip 10001 "New York"

Zip 10001 "New York"

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bioinformatics version 4.5
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ORF nucleotide sequence search using SW model

Match: 50.2729, 25153.2 : Search time 2511.8 seconds
(without alignments)
6.166 Million cell updates/sec

File: us09-sw-8779

Footprint sequence: 18

Sequence: 1-4-cccccagccagccatc 18

Sequencing table: IDENTITY, 90%

Gap: 150, gapopen: 1.0

Search: 900621 seqs, 12902619 residues

Total number of hits satisfying chosen parameters: 1661242

Minimum hit seq length: 1

Maximum hit seq length: 1000

Post processing: Minimum Match: 80

List top first 45 summaries

Database: 1

Rank	Score	Match	Length	Hit	Description
1	100.0	18	18	AAV0916	Antibody in antisense
2	100.0	14	14	AAV0916	Human secreted pro
3	100.0	14	14	AAV0916	Human secreted pro
4	100.0	14	14	AAV0916	Human secreted pro
5	100.0	14	14	AAV0916	Human secreted pro
6	100.0	14	14	AAV0916	Human secreted pro
7	100.0	14	14	AAV0916	Human secreted pro
8	100.0	14	14	AAV0916	Human secreted pro
9	100.0	14	14	AAV0916	Human secreted pro
10	100.0	14	14	AAV0916	Human secreted pro
11	100.0	14	14	AAV0916	Human secreted pro
12	100.0	14	14	AAV0916	Human secreted pro
13	100.0	14	14	AAV0916	Human secreted pro
14	100.0	14	14	AAV0916	Human secreted pro
15	100.0	14	14	AAV0916	Human secreted pro
16	100.0	14	14	AAV0916	Human secreted pro
17	100.0	14	14	AAV0916	Human secreted pro
18	100.0	14	14	AAV0916	Human secreted pro
19	100.0	14	14	AAV0916	Human secreted pro
20	100.0	14	14	AAV0916	Human secreted pro
21	100.0	14	14	AAV0916	Human secreted pro
22	100.0	14	14	AAV0916	Human secreted pro

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rank	Score	Match	Length	Hit	Description
1	100.0	18	18	AAV0916	Antibody in antisense
2	100.0	14	14	AAV0916	Human secreted pro
3	100.0	14	14	AAV0916	Human secreted pro
4	100.0	14	14	AAV0916	Human secreted pro
5	100.0	14	14	AAV0916	Human secreted pro
6	100.0	14	14	AAV0916	Human secreted pro
7	100.0	14	14	AAV0916	Human secreted pro
8	100.0	14	14	AAV0916	Human secreted pro
9	100.0	14	14	AAV0916	Human secreted pro
10	100.0	14	14	AAV0916	Human secreted pro
11	100.0	14	14	AAV0916	Human secreted pro
12	100.0	14	14	AAV0916	Human secreted pro
13	100.0	14	14	AAV0916	Human secreted pro
14	100.0	14	14	AAV0916	Human secreted pro
15	100.0	14	14	AAV0916	Human secreted pro
16	100.0	14	14	AAV0916	Human secreted pro
17	100.0	14	14	AAV0916	Human secreted pro
18	100.0	14	14	AAV0916	Human secreted pro
19	100.0	14	14	AAV0916	Human secreted pro
20	100.0	14	14	AAV0916	Human secreted pro
21	100.0	14	14	AAV0916	Human secreted pro
22	100.0	14	14	AAV0916	Human secreted pro

Rank	Score	Match	Length	Hit	Description
1	100.0	18	18	AAV0916	Antibody in antisense
2	100.0	14	14	AAV0916	Human secreted pro
3	100.0	14	14	AAV0916	Human secreted pro
4	100.0	14	14	AAV0916	Human secreted pro
5	100.0	14	14	AAV0916	Human secreted pro
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21	100.0	14	14	AAV0916	Human secreted pro
22	100.0	14	14	AAV0916	Human secreted pro

RESULTS

Rank	Score	Match	Length	Hit	Description
1	100.0	18	18	AAV0916	Antibody in antisense
2	100.0	14	14	AAV0916	Human secreted pro
3	100.0	14	14	AAV0916	Human secreted pro
4	100.0	14	14	AAV0916	Human secreted pro
5	100.0	14	14	AAV0916	Human secreted pro
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21	100.0	14	14	AAV0916	Human secreted pro
22	100.0	14	14	AAV0916	Human secreted pro

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As a coarse phosphor of choice, a phosphor of the BaF_2 composition, the BaF_2 crystal, is chosen as the "coarse phosphor" (see AAY-019). The BaF_2 crystal of choice is phosphor grade (see AAY-019) with the composition and structure of BaF_2 (see AAY-019). The phosphor grade of the BaF_2 expression is BaF_2 .

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Case	Age	Sex	Duration (yr)	Site	Histology	Immunohistochemistry	Molecular biology	Outcome	Comments
1	65	M	10	Rectum	Adenocarcinoma	+	+	Alive	
2	72	F	15	Rectum	Adenocarcinoma	+	+	Deceased	
3	68	M	8	Rectum	Adenocarcinoma	+	+	Alive	
4	70	F	12	Rectum	Adenocarcinoma	+	+	Deceased	
5	63	M	5	Rectum	Adenocarcinoma	+	+	Alive	
6	75	F	18	Rectum	Adenocarcinoma	+	+	Deceased	
7	60	M	7	Rectum	Adenocarcinoma	+	+	Alive	
8	71	F	14	Rectum	Adenocarcinoma	+	+	Deceased	
9	66	M	9	Rectum	Adenocarcinoma	+	+	Alive	
10	73	F	16	Rectum	Adenocarcinoma	+	+	Deceased	
11	64	M	6	Rectum	Adenocarcinoma	+	+	Alive	
12	74	F	17	Rectum	Adenocarcinoma	+	+	Deceased	
13	62	M	4	Rectum	Adenocarcinoma	+	+	Alive	
14	76	F	19	Rectum	Adenocarcinoma	+	+	Deceased	
15	61	M	3	Rectum	Adenocarcinoma	+	+	Alive	
16	77	F	20	Rectum	Adenocarcinoma	+	+	Deceased	
17	67	M	11	Rectum	Adenocarcinoma	+	+	Alive	
18	78	F	21	Rectum	Adenocarcinoma	+	+	Deceased	
19	69	M	13	Rectum	Adenocarcinoma	+	+	Alive	
20	79	F	22	Rectum	Adenocarcinoma	+	+	Deceased	

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (n = 10) and the intervention group (n = 10). The control group received a standard care (SC) protocol, while the intervention group received a SC protocol plus a 4-week intervention program. The intervention program consisted of a 4-week intervention program (IP) followed by a 4-week follow-up (FU) period. The intervention program was designed to improve the subjects' physical and psychological health. The subjects in the intervention group were asked to perform a series of exercises and to follow a specific diet. The subjects in the control group were asked to follow a standard care protocol. The subjects in the intervention group were asked to perform a series of exercises and to follow a specific diet. The subjects in the control group were asked to follow a standard care protocol. The subjects in the intervention group were asked to perform a series of exercises and to follow a specific diet. The subjects in the control group were asked to follow a standard care protocol. The subjects in the intervention group were asked to perform a series of exercises and to follow a specific diet.

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Mathematics

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Human and rat liver cytosol fractions were separated by sucrose density gradient centrifugation and the fractions were assayed for RNA polymerase activity.

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The diagram illustrates the experimental design. It shows a sequence of events: a subject is presented with a stimulus (a face), then a response is recorded (a button press), and finally, the subject is presented with a feedback stimulus (a face). The response is recorded by a computer system.

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(c) the present invention is related to a whole exon nucleic acid probes (SEN1),

(d) the present sequence is one such probe, the probes are useful for

(e) ready a methodology for product test, measuring and displaying gene

(f) expression in the samples derived from the human placenta, the probes are useful

(g) as a set of diagnostic and/or genetic markers.

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

Figure	Figure Description	Figure Type	Figure Content
Figure 1	Flowchart of the study design	Flowchart	Flowchart showing the study design, starting with 1000 participants, divided into two groups of 500 each. The first group is the control group, and the second group is the intervention group. The control group receives standard care, and the intervention group receives a combination of standard care and a new intervention. The study duration is 12 weeks, and the primary outcome is the change in blood pressure.
Figure 2	Baseline characteristics of the study population	Table	Table with 2 columns: Variable and Value. Rows include Age (mean), Sex (male/female), BMI (mean), and Blood pressure (mean).
Figure 3	Change in blood pressure over time	Line graph	Line graph showing the change in blood pressure (mmHg) over time (weeks) for the control group (n=500) and the intervention group (n=500). The control group shows a smaller decrease in blood pressure compared to the intervention group.
Figure 4	Change in blood pressure over time (adjusted for baseline characteristics)	Line graph	Line graph showing the change in blood pressure (mmHg) over time (weeks) for the control group (n=500) and the intervention group (n=500), adjusted for baseline characteristics. The intervention group shows a significantly larger decrease in blood pressure compared to the control group.
Figure 5	Change in blood pressure over time (adjusted for baseline characteristics and other factors)	Line graph	Line graph showing the change in blood pressure (mmHg) over time (weeks) for the control group (n=500) and the intervention group (n=500), adjusted for baseline characteristics and other factors. The intervention group shows a significantly larger decrease in blood pressure compared to the control group.
Figure 6	Change in blood pressure over time (adjusted for baseline characteristics and other factors, with 95% CI)	Line graph	Line graph showing the change in blood pressure (mmHg) over time (weeks) for the control group (n=500) and the intervention group (n=500), adjusted for baseline characteristics and other factors, with 95% CI. The intervention group shows a significantly larger decrease in blood pressure compared to the control group.
Figure 7	Change in blood pressure over time (adjusted for baseline characteristics and other factors, with 95% CI, and p-value)	Line graph	Line graph showing the change in blood pressure (mmHg) over time (weeks) for the control group (n=500) and the intervention group (n=500), adjusted for baseline characteristics and other factors, with 95% CI, and p-value. The intervention group shows a significantly larger decrease in blood pressure compared to the control group.
Figure 8	Change in blood pressure over time (adjusted for baseline characteristics and other factors, with 95% CI, and p-value, and subgroup analysis)	Line graph	Line graph showing the change in blood pressure (mmHg) over time (weeks) for the control group (n=500) and the intervention group (n=500), adjusted for baseline characteristics and other factors, with 95% CI, and p-value, and subgroup analysis. The intervention group shows a significantly larger decrease in blood pressure compared to the control group.
Figure 9	Change in blood pressure over time (adjusted for baseline characteristics and other factors, with 95% CI, and p-value, and subgroup analysis, and sensitivity analysis)	Line graph	Line graph showing the change in blood pressure (mmHg) over time (weeks) for the control group (n=500) and the intervention group (n=500), adjusted for baseline characteristics and other factors, with 95% CI, and p-value, and subgroup analysis, and sensitivity analysis. The intervention group shows a significantly larger decrease in blood pressure compared to the control group.
Figure 10	Change in blood pressure over time (adjusted for baseline characteristics and other factors, with 95% CI, and p-value, and subgroup analysis, and sensitivity analysis, and meta-analysis)	Line graph	Line graph showing the change in blood pressure (mmHg) over time (weeks) for the control group (n=500) and the intervention group (n=500), adjusted for baseline characteristics and other factors, with 95% CI, and p-value, and subgroup analysis, and sensitivity analysis, and meta-analysis. The intervention group shows a significantly larger decrease in blood pressure compared to the control group.

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NATIONAL INSTITUTE OF STANDARDS AND TECHNOLOGY

Abstract. We study the asymptotic behavior of the eigenvalues of the Dirac operator associated with the Dirac–Klein–Gordon system in the presence of a magnetic field. The results are obtained by means of the asymptotic expansion method.

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the present sequence especially a rat olfactory bulb receptor polypeptide coded by ϵ_1 . The protein is expressed specifically in myelin producing cells, and is a member of the α_1 family of proteins, which is distinct

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

[illegible]

TABLE 1. *Mean values of the variables used in the analysis*



XX Liver, breast and lymphomas); behavioral disorders (tremor/ticks
XX syndrome); musculo-skeletal disorders (arthritis, edema, tendonitis);
XX renal disorders (nephritic syndrome, glomerulonephritis); metastases of
XX malignancies and related disorders (osteoma, multiple myeloma); and
XX infections caused by bacteria, viruses, fungi and parasites. PKK is also
XX useful for screening therapeutic compounds. PKK is used as an antigen in
XX a vaccine to raise an immune response against infectious disease. PKK
XX nucleic acids are useful in gene therapy.

SD Sequence 2946 RP; 864 A; 656 V; 668 G; 728 T; 0 other;

Query Match: 82.2%; Score 14.8; Pos 22; Length 2946;
Best Local Similarity: 88.9%; Pos 1; Length 2946;
Matches 16; Conservation: 3; Mismatches 2; Indels 0; Gaps 0;

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RESULT 13
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